



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/678,023

Source: FW/6

Date Processed by STIC: 11/24/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~
~~VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND~~
~~TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:~~

~~<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>~~

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby,
Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/678,023

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 ☒ Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 ☐ PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 ☐ Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:

(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO. where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 ☐ Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.

<210> sequence id number
<400> sequence id number
000

- 9 ☐ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.

Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 ☐ Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.

- 11 ☐ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.

Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 ☐ PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 ☐ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 11/24/2004

PATENT APPLICATION: US/09/678,023

TIME: 12:32:34

Input Set : A:\5.1158 Div 1 Sequence Listing.txt

Output Set: N:\CRF4\11242004\I678023.raw

SEQUENCE LISTING

**Does Not Comply
Corrected Diskette Needed**

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: KAWASAKI, Hideki

7 TOKAI, Masaya

8 KIKUCHI, Yasuhiro

9 OUCHI, Kozo

11 (ii) TITLE OF INVENTION: DNA ENCODING PROTEIN COMPLEMENTING

12 YEAST

13 LOW TEMPERATURE-SENSITIVE FERMENTABILITY

15 (iii) NUMBER OF SEQUENCES: 2

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO

19 (B) STREET: 30 Rockefeller Plaza

20 (C) CITY: New York

21 (D) STATE: New York

22 (E) COUNTRY: U.S.A.

23 (F) ZIP: 10112-3801

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Diskette - 3.50 inch, 1440 Kb storage.

29 (B) COMPUTER: IBM PS/V

30 (C) OPERATING SYSTEM: MS-DOS Ver3.30

31 (D) SOFTWARE: PATENT AID Ver1.0

33 (vi) CURRENT APPLICATION DATA:

C--> 34 (A) APPLICATION NUMBER: US/09/678,023

C--> 35 (B) FILING DATE: 04-Oct-2000

41 (vii) PRIOR APPLICATION DATA:

W--> 38 (A) APPLICATION NUMBER: 08/894,344

39 (B) FILING DATE: 15-AUGUST-1997

W--> 42 (A) APPLICATION NUMBER: JP343700/95

43 (B) FILING DATE: 28-DECEMBER-1995

W--> 44 (A) APPLICATION NUMBER: PCT/JP96/03862

45 (B) FILING DATE: 27-DECEMBER-1996

47 (viii) ATTORNEY/AGENT INFORMATION:

48 (A) NAME: Perry, Lawrence S.

49 (B) REGISTRATION NUMBER: 31865

51 (ix) TELECOMMUNICATION INFORMATION:

52 (A) TELEPHONE: 212-218-2100

53 (B) TELEFAX: 212-218-2200

PP-4-9

ERRORED SEQUENCES

466 (2) INFORMATION FOR SEQ ID NO: 2 :

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DATE: 11/24/2004

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Input Set : A:\5.1158 Div 1 Sequence Listing.txt

Output Set: N:\CRF4\11242004\I678023.raw

```

468      (i) SEQUENCE CHARACTERISTICS:
469          (A) LENGTH: 2958 amino acids
470          (B) TYPE: amino acid
471          (D) TOPOLOGY: linear
473      (ii) MOLECULE TYPE: protein
475      (vi) ORIGINAL SOURCE:
476          (A) ORGANISM: Saccharomyces cerevisiae
477          (B) STRAIN: X2180-1B
479      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2
481  Met Glu Ala Ile Ser Gln Leu Arg Gly Val Pro Leu Thr His Gln Lys
483      1              5              10              15
485  Asp Phe Ser Trp Val Phe Leu Val Asp Trp Ile Leu Thr Val Val Val
487              20              25              30
489  Cys Leu Thr Met Ile Phe Tyr Met Gly Arg Ile Tyr Ala Tyr Leu Val
491              35              40              45
493  Ser Phe Ile Leu Glu Trp Leu Leu Trp Lys Arg Ala Lys Ile Lys Ile
495              50              55              60
497  Asn Val Glu Thr Leu Arg Val Ser Leu Leu Gly Gly Arg Ile His Phe
499              65              70              75              80
501  Lys Asn Leu Ser Val Ile His Lys Asp Tyr Thr Ile Ser Val Leu Glu
503              85              90              95
505  Gly Ser Leu Thr Trp Lys Tyr Trp Leu Leu Asn Cys Arg Lys Ala Glu
507              100             105             110
509  Leu Ile Glu Asn Asn Lys Ser Ser Ser Gly Lys Lys Ala Lys Leu Pro
511              115             120             125
513  Cys Lys Ile Ser Val Glu Cys Glu Gly Leu Glu Ile Phe Ile Tyr Asn
515              130             135             140
517  Arg Thr Val Ala Tyr Asp Asn Val Ile Asn Leu Leu Ser Lys Asp Glu
519              145             150             155             160
521  Arg Asp Lys Phe Glu Lys Tyr Leu Asn Glu His Ser Phe Pro Glu Pro
523              165             170             175
525  Phe Ser Asp Gly Ser Ser Ala Asp Lys Leu Asp Glu Asp Leu Ser Glu
527              180             185             190
529  Ser Ala Tyr Thr Thr Asn Ser Asp Ala Ser Ile Val Asn Asp Arg Asp
531              195             200             205
533  Tyr Gln Glu Thr Asp Ile Gly Lys His Pro Lys Leu Leu Met Phe Leu
535              210             215             220
537  Pro Ile Glu Leu Lys Phe Ser Arg Gly Ser Leu Leu Leu Gly Asn Lys
539              225             230             235             240
541  Phe Thr Pro Ser Val Met Ile Leu Ser Tyr Glu Ser Gly Lys Gly Ile
543              245             250             255
545  Ile Asp Val Leu Pro Pro Lys Glu Arg Leu Asp Leu Tyr Arg Asn Lys
547              260             265             270
549  Thr Gln Met Glu Phe Lys Asn Phe Glu Ile Ser Ile Lys Gln Asn Ile
551              275             280             285
553  Gly Tyr Asp Asp Ala Ile Gly Leu Lys Phe Lys Ile Asp Arg Gly Lys
555              290             295             300
557  Val Ser Lys Leu Trp Lys Thr Phe Val Arg Val Phe Gln Ile Val Thr
559              305             310             315             320

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```

561 Lys Pro Val Val Pro Lys Lys Thr Lys Lys Ser Ala Gly Thr Ser Asp
563                               325                               330                               335
565 Asp Asn Phe Tyr His Lys Trp Lys Gly Leu Ser Leu Tyr Lys Ala Ser
567                               340                               345                               350
569 Ala Gly Asp Ala Lys Ala Ser Asp Leu Asp Asp Val Glu Phe Asp Leu
571                               355                               360                               365
573 Thr Asn His Glu Tyr Ala Lys Phe Thr Ser Ile Leu Lys Cys Pro Lys
575                               370                               375                               380
577 Val Thr Ile Ala Tyr Asp Val Asp Val Pro Gly Val Val Pro His Gly
579                               385                               390                               395                               400
581 Ala His Pro Thr Ile Pro Asp Ile Asp Gly Pro Asp Val Gly Asn Asn
583                               405                               410                               415
585 Gly Ala Pro Pro Asp Phe Ala Leu Asp Val Gln Ile His Gly Gly Ser
587                               420                               425                               430
589 Ile Cys Tyr Gly Pro Trp Ala Gln Arg Gln Val Ser His Leu Gln Arg
591                               435                               440                               445
593 Val Leu Ser Pro Val Val Ser Arg Thr Ala Lys Pro Ile Lys Lys Leu
595                               450                               455                               460
597 Pro Pro Gly Ser Arg Arg Ile Tyr Thr Leu Phe Arg Met Asn Ile Ser
599                               465                               470                               475                               480
601 Ile Met Glu Asp Thr Thr Trp Arg Ile Pro Thr Arg Glu Ser Ser Lys
603                               485                               490                               495
605 Asp Pro Glu Phe Leu Lys His Tyr Lys Glu Thr Asn Glu Glu Tyr Arg
607                               500                               505                               510
609 Pro Phe Gly Trp Met Asp Leu Arg Phe Cys Lys Asp Thr Tyr Ala Asn
611                               515                               520                               525
613 Phe Asn Ile Ser Val Cys Pro Thr Val Gln Gly Phe Gln Asn Asn Phe
615                               530                               535                               540
617 His Val His Phe Leu Glu Thr Glu Ile Arg Ser Ser Val Asn His Asp
619                               545                               550                               555                               560
621 Ile Leu Leu Lys Ser Lys Val Phe Asp Ile Asp Gly Asp Ile Gly Tyr
623                               565                               570                               575
625 Pro Leu Gly Trp Asn Ser Lys Ala Ile Trp Ile Ile Asn Met Lys Ser
627                               580                               585                               590
629 Glu Gln Leu Glu Ala Phe Leu Leu Arg Glu His Ile Thr Leu Val Ala
631                               595                               600                               605
633 Asp Thr Leu Ser Asp Phe Ser Ala Gly Asp Pro Thr Pro Tyr Glu Leu
635                               610                               615                               620
637 Phe Arg Pro Phe Val Tyr Lys Val Asn Trp Glu Met Glu Gly Tyr Ser
639                               625                               630                               635                               640
641 Ile Tyr Leu Asn Val Asn Asp His Asn Ile Val Asn Asn Pro Leu Asp
643                               645                               650                               655
645 Phe Asn Glu Asn Cys Tyr Leu Ser Leu His Gly Asp Lys Leu Ser Ile
647                               660                               665                               670
649 Asp Val Thr Val Pro Arg Glu Ser Ile Leu Gly Thr Tyr Thr Asp Met
651                               675                               680                               685
653 Ser Tyr Glu Ile Ser Thr Pro Met Phe Arg Met Met Leu Asn Thr Pro
655                               690                               695                               700
657 Pro Trp Asn Thr Leu Asn Glu Phe Met Lys His Lys Glu Val Gly Arg

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```

659 705 710 715 720
661 Ala Tyr Asp Phe Thr Ile Lys Gly Ser Tyr Leu Leu Tyr Ser Glu Leu
663 725 730 735
665 Asp Ile Asp Asn Val Asp Thr Leu Val Ile Glu Cys Asn Ser Lys Ser
667 740 745 750
669 Thr Val Leu His Cys Tyr Gly Phe Val Met Arg Tyr Leu Thr Asn Val
671 755 760 765
673 Lys Met Asn Tyr Phe Gly Glu Phe Phe Asn Phe Val Thr Ser Glu Glu
675 770 775 780
677 Tyr Thr Gly Val Leu Gly Ala Arg Glu Val Gly Asp Val Thr Thr Lys
679 785 790 795 800
681 Ser Ser Val Ala Asp Leu Ala Ser Thr Val Asp Ser Gly Tyr Gln Asn
683 805 810 815
685 Ser Ser Leu Lys Asn Glu Ser Glu Asp Lys Gly Pro Met Lys Arg Ser
687 820 825 830
689 Asp Leu Lys Arg Thr Thr Asn Glu Thr Asp Ile Trp Phe Thr Phe Ser
691 835 840 845
693 Val Trp Asp Gly Ala Leu Ile Leu Pro Glu Thr Ile Tyr Ser Phe Asp
695 850 855 860
697 Pro Cys Ile Ala Leu His Phe Ala Glu Leu Val Val Asp Phe Arg Ser
699 865 870 875 880
701 Cys Asn Tyr Tyr Met Asp Ile Met Ala Val Leu Asn Gly Thr Ser Ile
703 885 890 895
705 Lys Arg His Val Ser Lys Gln Ile Asn Glu Val Phe Asp Phe Ile Arg
707 900 905 910
709 Arg Asn Asn Gly Ala Asp Glu Gln Glu His Gly Leu Leu Ser Asp Leu
711 915 920 925
713 Thr Ile His Gly His Arg Met Tyr Gly Leu Pro Pro Thr Glu Pro Thr
715 930 935 940
717 Tyr Phe Cys Gln Trp Asp Ile Asn Leu Gly Asp Leu Cys Ile Asp Ser
719 945 950 955 960
721 Asp Ile Glu Phe Ile Lys Gly Phe Phe Asn Ser Phe Tyr Lys Ile Gly
723 965 970 975
725 Phe Gly Tyr Asn Asp Leu Glu Asn Ile Leu Leu Tyr Asp Thr Glu Thr
727 980 985 990
729 Ile Asn Asp Met Thr Ser Leu Thr Val His Val Glu Lys Ile Arg Ile
731 995 1000 1005
733 Gly Leu Lys Asp Pro Val Met Lys Ser Gln Ser Val Ile Ser Ala Glu
735 1010 1015 1020
737 Ser Ile Leu Phe Thr Leu Ile Asp Phe Glu Asn Glu Lys Tyr Ser Gln
E--> 739 1025 1030 1035 1040
E--> 740 1040
741 Arg Ile Asp Val Lys Ile Pro Lys Leu Thr Ile Ser Leu Asn Cys Val
E--> 743 1045 1050 1055
745 Met Gly Asp Gly Val Asp Thr Ser Phe Leu Lys Phe Glu Thr Lys Leu
E--> 747 1060 1065 1070
749 Arg Phe Thr Asn Phe Glu Gln Tyr Lys Asp Ile Asp Lys Lys Arg Ser
E--> 751 1075 1080 1085
753 Glu Gln Arg Arg Tyr Ile Thr Ile His Asp Ser Pro Tyr His Arg Cys

```

See item 3 on Error Summary Sheet.

file://C:\CRF4\Outhold\VsrI678023.htm

*Please
verify your
amino acid
numbering. Make
sure the numbers are
under their respective amino acids. 11/24/04*

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```

E--> 755      1090      1095      1100
      757  Pro Phe Leu Leu Pro Leu Phe Tyr Gln Asp Ser Asp Thr Tyr Gln Asn
E--> 759      1105      1110      1115      1120
      761  Leu Tyr Gly Ala Ile Ala Pro Ser Ser Ser Ile Pro Thr Leu Pro Leu
E--> 763      1125      1130      1135
      765  Pro Thr Leu Pro Asp Thr Ile Asp Tyr Ile Ile Glu Asp Ile Val Gly
E--> 767      1140      1145      1150
      769  Glu Tyr Ala Thr Leu Leu Glu Thr Thr Asn Pro Phe Lys Asn Ile Phe
E--> 771      1155      1160      1165
      773  Ala Glu Thr Pro Ser Thr Met Glu Pro Ser Arg Ala Ser Phe Ser Glu
E--> 775      1170      1175      1180
      777  Asp Asp Asn Asp Glu Glu Ala Asp Pro Ser Ser Phe Lys Pro Val Ala
E--> 779      1185      1190      1195      1200
      781  Phe Thr Glu Asp Arg Asn His Glu Arg Asp Asn Tyr Val Val Asp Val
E--> 783      1205      1210      1215
      785  Ser Tyr Ile Leu Leu Asp Val Asp Pro Leu Leu Phe Ile Phe Ala Lys
E--> 787      1220      1225      1230
      789  Ser Leu Leu Glu Gln Leu Tyr Ser Glu Asn Met Val Gln Val Leu Asp
E--> 791      1235      1240      1245
      793  Asp Ile Glu Ile Gly Ile Val Lys Arg Leu Ser Asn Leu Gln Glu Gly
E--> 795      1250      1255      1260
      797  Ile Thr Ser Ile Ser Asn Ile Asp Ile His Ile Ala Tyr Leu Asn Leu
E--> 799      1265      1270      1275      1280
      801  Ile Trp Gln Glu Thr Gly Glu Glu Gly Phe Glu Leu Tyr Leu Asp Arg
E--> 803      1285      1290      1295
      805  Ile Asp Tyr Gln Met Ser Glu Lys Ser Leu Glu Lys Asn Arg Thr Asn
E--> 807      1300      1305      1310
      809  Lys Leu Leu Glu Val Ala Ala Leu Ala Lys Val Lys Thr Val Arg Val
E--> 811      1315      1320      1325
      813  Thr Val Asn Gln Lys Lys Asn Pro Asp Leu Ser Glu Asp Arg Pro Pro
E--> 815      1330      1335      1340
      817  Ala Leu Ser Leu Gly Ile Glu Gly Phe Glu Val Trp Ser Ser Thr Glu
E--> 819      1345      1350      1355      1360
      821  Asp Arg Gln Val Asn Ser Leu Asn Leu Thr Ser Ser Asp Ile Thr Ile
E--> 823      1365      1370      1375
      825  Asp Glu Ser Gln Met Glu Trp Leu Phe Glu Tyr Cys Ser Asp Gln Gly
E--> 827      1380      1385      1390
      829  Asn Leu Ile Gln Glu Val Cys Thr Ser Phe Asn Ser Ile Gln Asn Thr
E--> 831      1395      1400      1405
      833  Arg Ser Asn Ser Lys Thr Glu Leu Ile Ser Lys Leu Thr Ala Ala Ser
E--> 835      1410      1415      1420
      837  Glu Tyr Tyr Gln Ile Ser His Asp Pro Tyr Val Ile Thr Lys Pro Ala
E--> 839      1425      1430      1435      1440
      841  Phe Ile Met Arg Leu Ser Lys Gly His Val Arg Glu Asn Arg Ser Trp
E--> 843      1445      1450      1455
      845  Lys Ile Ile Thr Arg Leu Arg His Ile Leu Thr Tyr Leu Pro Asp Asp
E--> 847      1460      1465      1470
      849  Trp Gln Ser Asn Ile Asp Glu Val Leu Lys Glu Lys Lys Tyr Thr Ser
E--> 851      1475      1480      1485

```

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```

      853 Ala Lys Asp Ala Lys Asn Ile Phe Met Ser Val Phe Ser Thr Trp Arg
E--> 855      1490      1495      1500
      857 Asn Trp Glu Phe Ser Asp Val Ala Arg Ser Tyr Ile Tyr Gly Lys Leu
E--> 859      1505      1510      1515      1520
      861 Phe Thr Ala Glu Asn Glu Lys His Lys Gln Asn Leu Ile Lys Lys Leu
E--> 863      1525      1530      1535
      865 Leu Lys Cys Thr Met Gly Ser Phe Tyr Leu Thr Val Tyr Gly Glu Gly
E--> 867      1540      1545      1550
      869 Tyr Glu Val Glu His Asn Phe Val Val Ala Asp Ala Asn Leu Val Val
E--> 871      1555      1560      1565
      873 Asp Leu Thr Pro Pro Val Thr Ser Leu Pro Ser Asn Arg Glu Glu Thr
E--> 875      1570      1575      1580
      877 Ile Glu Ile Thr Gly Arg Val Gly Ser Val Lys Gly Lys Phe Ser Asp
E--> 879      1585      1590      1595      1600
      881 Arg Leu Leu Lys Leu Gln Asp Leu Ile Pro Leu Ile Ala Ala Val Gly
E--> 883      1605      1610      1615
      885 Glu Asp Asp Lys Ser Asp Pro Lys Lys Glu Leu Ser Lys Gln Phe Lys
E--> 887      1620      1625      1630
      889 Met Asn Thr Val Leu Leu Val Asp Lys Ser Glu Leu Gln Leu Val Met
E--> 891      1635      1640      1645
      893 Asp Gln Thr Lys Leu Met Ser Arg Thr Val Gly Gly Arg Val Ser Leu
E--> 895      1650      1655      1660
      897 Leu Trp Glu Asn Leu Lys Asp Ser Thr Ser Gln Ala Gly Ser Leu Val
E--> 899      1665      1670      1675      1680
      901 Ile Phe Ser Gln Lys Ser Glu Val Trp Leu Lys His Thr Ser Val Ile
E--> 903      1685      1690      1695
      905 Leu Gly Glu Ala Gln Leu Arg Asp Phe Ser Val Leu Ala Thr Thr Glu
E--> 907      1700      1705      1710
      909 Ala Trp Ser His Lys Pro Thr Ile Leu Ile Asn Asn Gln Cys Ala Asp
E--> 911      1715      1720      1725
      913 Leu His Phe Arg Ala Met Ser Ser Thr Glu Gln Leu Val Thr Ala Ile
E--> 915      1730      1735      1740
      917 Thr Glu Ile Arg Glu Ser Leu Met Met Ile Lys Glu Arg Ile Lys Phe
E--> 919      1745      1750      1755      1760
      921 Lys Pro Lys Ser Lys Lys Lys Ser Gln Phe Val Asp Gln Lys Ile Asn
E--> 923      1765      1770      1775
      925 Thr Val Leu Ser Cys Tyr Phe Ser Asn Val Ser Ser Glu Val Met Pro
E--> 927      1780      1785      1790
      929 Leu Ser Pro Phe Tyr Ile Arg His Glu Ala Lys Gln Leu Asp Ile Tyr
E--> 931      1795      1800      1805
      933 Phe Asn Lys Phe Gly Ser Asn Glu Ile Leu Leu Ser Ile Trp Asp Thr
E--> 935      1810      1815      1820
      937 Asp Phe Phe Met Thr Ser His Gln Thr Lys Glu Gln Tyr Leu Arg Phe
E--> 939      1825      1830      1835      1840
      941 Ser Phe Gly Asp Ile Glu Ile Lys Gly Gly Ile Ser Arg Glu Gly Tyr
E--> 943      1845      1850      1855
      945 Ser Leu Ile Asn Val Asp Ile Ser Ile Ser Met Ile Lys Leu Thr Phe
E--> 947      1860      1865      1870
      949 Ser Glu Pro Arg Arg Ile Val Asn Ser Phe Leu Gln Asp Glu Lys Leu

```

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```

E--> 951      1875      1880      1885
      953 Ala Ser Gln Gly Ile Asn Leu Leu Tyr Ser Leu Lys Pro Leu Phe Phe
E--> 955      1890      1895      1900
      957 Ser Ser Asn Leu Pro Lys Lys Glu Lys Gln Ala Pro Ser Ile Met Ile
E--> 959      1905      1910      1915      1920
      961 Asn Trp Thr Leu Asp Thr Ser Ile Thr Tyr Phe Gly Val Leu Val Pro
E--> 963      1925      1930      1935
      965 Val Ala Ser Thr Tyr Phe Val Phe Glu Leu His Met Leu Leu Leu Ser
E--> 966      1940 1940 1945 1945 1950 1950
      968 Leu Thr Asn Thr Asn Asn Gly Met Leu Pro Glu Glu Thr Lys Val Thr
E--> 970      1955      1960      1965
      972 Gly Gln Phe Ser Ile Glu Asn Ile Leu Phe Leu Ile Lys Glu Arg Ser
E--> 974      1970      1975      1980
      976 Leu Pro Ile Gly Leu Ser Lys Leu Leu Asp Phe Ser Ile Lys Val Ser
E--> 978      1985      1990      1995      2000
      980 Thr Leu Gln Arg Thr Val Asp Thr Glu Gln Ser Phe Gln Val Glu Ser
E--> 982      2005      2010      2015
      984 Ser His Phe Arg Val Cys Leu Ser Pro Asp Ser Leu Leu Arg Leu Met
E--> 986      2020      2025      2030
      988 Trp Gly Ala His Lys Leu Leu Asp Leu Ser His Tyr Tyr Ser Arg Arg
E--> 990      2035      2040      2045
      992 His Ala Pro Asn Ile Trp Asn Thr Lys Met Phe Thr Gly Lys Ser Asp
E--> 994      2050      2055      2060
      996 Lys Ser Lys Glu Met Pro Ile Asn Phe Arg Ser Ile His Ile Leu Ser
E--> 998      2065      2070      2075      2080
      1000 Tyr Lys Phe Cys Ile Gly Trp Ile Phe Gln Tyr Gly Ala Gly Ser Asn
E--> 1002      2085      2090      2095
      1004 Pro Gly Leu Met Leu Gly Tyr Asn Arg Leu Phe Ser Ala Tyr Glu Lys
E--> 1006      2100      2105      2110
      1008 Asp Phe Gly Lys Phe Thr Val Val Asp Ala Phe Phe Ser Val Ala Asn
E--> 1010      2115      2120      2125
      1012 Gly Asn Thr Ser Ser Thr Phe Phe Ser Glu Gly Asn Glu Lys Asp Lys
E--> 1014      2130      2135      2140
      1016 Tyr Asn Arg Ser Phe Leu Pro Asn Met Gln Ile Ser Tyr Trp Phe Lys
E--> 1018      2145      2150      2155      2160
      1020 Arg Cys Gly Glu Leu Lys Asp Trp Phe Phe Arg Phe His Gly Glu Ala
E--> 1022      2165      2170      2175
      1024 Leu Asp Val Asn Phe Val Pro Ser Phe Met Asp Val Ile Glu Ser Thr
E--> 1026      2180      2185      2190
      1028 Leu Gln Ser Met Arg Ala Phe Gln Glu Leu Lys Lys Asn Ile Leu Asp
E--> 1030      2195      2200      2205
      1032 Val Ser Glu Ser Leu Arg Ala Glu Asn Asp Asn Ser Tyr Ala Ser Thr
E--> 1034      2210      2215      2220
      1036 Ser Val Glu Ser Ala Ser Ser Ser Leu Ala Pro Phe Leu Asp Asn Ile
E--> 1038      2225      2230      2235      2240
      1040 Arg Ser Val Asn Ser Asn Phe Lys Tyr Asp Gly Gly Val Phe Arg Val
E--> 1042      2245      2250      2255
      1044 Tyr Thr Tyr Glu Asp Ile Glu Thr Lys Ser Glu Pro Ser Phe Glu Ile
E--> 1046      2260      2265      2270

```

← please
correct
this line
and
following
lines

RAW SEQUENCE LISTING

DATE: 11/24/2004

PATENT APPLICATION: US/09/678,023

TIME: 12:32:34

Input Set : A:\5.1158 Div 1 Sequence Listing.txt

Output Set: N:\CRF4\11242004\I678023.raw

```

1048 Lys Ser Pro Val Val Thr Ile Asn Cys Thr Tyr Lys His Asp Glu Asp
E--> 1050      2275      2280      2285
1052 Lys Val Lys Pro His Lys Phe Arg Thr Leu Ile Thr Val Asp Pro Thr
E--> 1054      2290      2295      2300
1056 His Asn Thr Leu Tyr Ala Gly Cys Ala Pro Leu Leu Met Glu Phe Ser
E--> 1058      2305      2310      2315      2320
1060 Glu Ser Leu Gln Lys Met Ile Lys Lys His Ser Thr Asp Glu Lys Pro
E--> 1062      2325      2330      2335
1064 Asn Phe Thr Lys Pro Ser Ser Gln Asn Val Asp Tyr Lys Arg Leu Leu
E--> 1066      2340      2345      2350
1068 Asp Gln Phe Asp Val Ala Val Lys Leu Thr Ser Ala Lys Gln Gln Leu
E--> 1070      2355      2360      2365
1072 Ser Leu Ser Cys Glu Pro Lys Ala Lys Val Gln Ala Asp Val Gly Phe
E--> 1074      2370      2375      2380
1076 Glu Ser Phe Leu Phe Ser Met Ala Thr Asn Glu Phe Asp Ser Glu Gln
E--> 1078      2385      2390      2395      2400
1080 Pro Leu Glu Phe Ser Leu Thr Leu Glu His Thr Lys Ala Ser Ile Lys
E--> 1082      2405      2410      2415
1084 His Ile Phe Ser Arg Glu Val Ser Thr Ser Phe Glu Val Gly Phe Met
E--> 1086      2420      2425      2430
1088 Asp Leu Thr Leu Leu Phe Thr His Pro Asp Val Ile Ser Met Tyr Gly
E--> 1090      2435      2440      2445
1092 Thr Gly Leu Val Ser Asp Leu Ser Val Phe Phe Asn Val Lys Gln Leu
E--> 1094      2450      2455      2460
1096 Gln Asn Leu Tyr Leu Phe Leu Asp Ile Trp Arg Phe Ser Ser Ile Leu
E--> 1098      2465      2470      2475      2480
1100 His Thr Arg Pro Val Gln Arg Thr Val Asn Lys Glu Ile Glu Met Ser
E--> 1102      2485      2490      2495
1104 Ser Leu Thr Ser Thr Asn Tyr Ala Asp Ala Gly Thr Glu Ile Pro Trp
E--> 1106      2500      2505      2510
1108 Cys Phe Thr Leu Ile Phe Thr Asn Val Ser Gly Asp Val Asp Leu Gly
E--> 1110      2515      2520      2525
1112 Pro Ser Leu Gly Met Ile Ser Leu Arg Thr Gln Arg Thr Trp Leu Ala
E--> 1114      2530      2535      2540
1116 Thr Asp His Tyr Asn Glu Lys Arg Gln Leu Leu His Ala Phe Thr Asp
E--> 1118      2545      2550      2555      2560
1120 Gly Ile Ser Leu Thr Ser Glu Gly Arg Leu Ser Gly Leu Phe Glu Val
E--> 1122      2565      2570      2575
1124 Ala Asn Ala Ser Trp Leu Ser Glu Val Lys Trp Pro Pro Glu Lys Ser
E--> 1126      2580      2585      2590
1128 Lys Asn Thr His Pro Leu Val Ser Thr Ser Leu Asn Ile Asp Asp Ile
E--> 1130      2595      2600      2605
1132 Ala Val Lys Ala Ala Phe Asp Tyr His Met Phe Leu Ile Gly Thr Ile
E--> 1134      2610      2615      2620
1136 Ser Asn Ile His Phe His Leu His Asn Glu Lys Asp Ala Lys Gly Val
E--> 1138      2625      2630      2635      2640
1140 Leu Pro Asp Leu Leu Gln Val Ser Phe Ser Ser Asp Glu Ile Ile Leu
E--> 1142      2645      2650      2655
1144 Ser Ser Thr Ala Leu Val Val Ala Asn Ile Leu Asp Ile Tyr Asn Thr

```

RAW SEQUENCE LISTING

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Input Set : A:\5.1158 Div 1 Sequence Listing.txt

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```

E--> 1146          2660          2665          2670
      1148 Ile Val Arg Met Arg Gln Asp Asn Lys Ile Ser Tyr Met Glu Thr Leu
E--> 1150          2675          2680          2685
      1152 Arg Asp Ser Asn Pro Gly Glu Ser Arg Gln Pro Ile Leu Tyr Lys Asp
E--> 1154          2690          2695          2700
      1156 Ile Leu Arg Ser Leu Lys Leu Leu Arg Thr Asp Leu Ser Val Asn Ile
E--> 1158          2705          2710          2715          2720
      1160 Ser Ser Ser Lys Val Gln Ile Ser Pro Ile Ser Leu Phe Asp Val Glu
E--> 1162          2725          2730          2735
      1164 Val Leu Val Ile Arg Ile Asp Lys Val Ser Ile Arg Ser Glu Thr His
E--> 1166          2740          2745          2750
      1168 Ser Gly Lys Lys Leu Lys Thr Asp Leu Gln Leu Gln Val Leu Asp Val
E--> 1170          2755          2760          2765
      1172 Ser Ala Ala Leu Ser Thr Ser Lys Glu Glu Leu Asp Glu Glu Val Gly
E--> 1174          2770          2775          2780
      1176 Ala Ser Ile Ala Ile Asp Asp Tyr Met His Tyr Ala Ser Lys Ile Val
E--> 1178          2785          2790          2795          2800
      1180 Gly Gly Thr Ile Ile Asp Ile Pro Lys Leu Ala Val His Met Thr Thr
E--> 1182          2805          2810          2815
      1184 Leu Gln Glu Glu Lys Thr Asn Asn Leu Glu Tyr Leu Phe Ala Cys Ser
E--> 1186          2820          2825          2830
      1188 Phe Ser Asp Lys Ile Ser Val Arg Trp Asn Leu Gly Pro Val Asp Phe
E--> 1190          2835          2840          2845
      1192 Ile Lys Glu Met Trp Thr Thr His Val Lys Ala Leu Ala Val Arg Arg
E--> 1194          2850          2855          2860
      1196 Ser Gln Val Ala Asn Ile Ser Phe Gly Gln Thr Glu Glu Glu Leu Glu
E--> 1198          2865          2870          2875          2880
      1200 Glu Ser Ile Lys Lys Glu Glu Ala Ala Ser Lys Phe Asn Tyr Ile Ala
E--> 1202          2885          2890          2895
      1204 Leu Glu Glu Pro Gln Ile Glu Val Pro Gln Ile Arg Asp Leu Gly Asp
E--> 1206          2900          2905          2910
      1208 Ala Thr Pro Pro Met Glu Trp Phe Gly Val Asn Arg Lys Lys Phe Pro
E--> 1210          2915          2920          2925
      1212 Lys Phe Thr His Gln Thr Ala Val Ile Pro Val Gln Lys Leu Val Tyr
E--> 1214          2930          2935          2940
      1216 Leu Ala Glu Lys Gln Tyr Val Lys Ile Leu Asp Asp Thr His
E--> 1218          2945          2950          2955

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/678,023

DATE: 11/24/2004

TIME: 12:32:35

Input Set : A:\5.1158 Div 1 Sequence Listing.txt

Output Set: N:\CRF4\11242004\I678023.raw

L:34 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:35 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:44 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:60 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:739 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2